

SEQUENCE LISTING

<110> Hitz, William
Sebastian, Scott
Grace, John
Streit, Leon

<120> SOYBEAN PLANT PRODUCING SEEDS WITH REDUCED LEVELS OF RAFFINOSE
SACCHARIDES AND PHYTIC ACID

<130> BB-1077-C

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<150> 08/835,751

<151> APRIL 8, 1997

<150> PCT/US98/06822

<151> APRIL 7, 1998

<160> 16

<170> Microsoft Office 97

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<211> 1760

<212> DNA

<213> Glycine max

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<212> PRT

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<400> 2

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Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
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His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
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Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
100 105 110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
290 295 300

Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
305 310 315 320

Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
325 330 335

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
 340 345 350
 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
 355 360 365
 Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
 370 375 380
 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
 385 390 395 400
 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu
 405 410 415
 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
 420 425 430
 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Phe Lys Ala Glu
 435 440 445
 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
 450 455 460
 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
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 Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
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 Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
 500 505 510

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 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic oligonucleotide

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<210> 4
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 4
 aaggaaaaaa gcggccgctc acttgctacg gagaatcat 39

<210> 5
 <211> 1533
 <212> DNA
 <213> Glycine max

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 cagtggattg tcaaacccaa atctgtcaaa tacgaattta aaaccaacat ccatgttcct 180
 aaattagggt taatgcttgt gggttgggtt ggaaacaacg gctcaaccct caccggtggt 240
 gttattgcta accgagaggg catttcatgg gctacaaagg acaagattca acaagccaat 300

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 <212> PRT
 <213> Glycine max

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 20 25 30
 His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
 35 40 45
 Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
 50 55 60
 Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
 65 70 75 80
 Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
 85 90 95
 Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
 100 105 110
 Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
 115 120 125
 Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
 130 135 140
 Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
 145 150 155 160
 Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
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 Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
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 Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
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<400> 7
cgtaggggac agcaag

16

<210> 8
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 8
cgtaggggac agcaat

16

<210> 9
<211> 1533
<212> DNA
<213> Glycine max

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ccagagaata acatgattct cgagtacaag tga 1533

<210> 10
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<212> PRT
<213> Glycine max

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His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
35 40 45
Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
 65 70 75 80
 Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
 85 90 95
 Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
 100 105 110
 Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
 115 120 125
 Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
 130 135 140
 Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
 145 150 155 160
 Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
 165 170 175
 Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
 180 185 190
 Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
 195 200 205
 Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
 210 215 220
 Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
 225 230 235 240
 Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
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 Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
 260 265 270
 Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
 275 280 285
 Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
 290 295 300
 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
 305 310 315 320
 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
 325 330 335
 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
 340 345 350
 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
 355 360 365
 Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
 370 375 380
 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
 385 390 395 400
 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu
 405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
 420 425 430
 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Phe Lys Ala Glu
 435 440 445
 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
 450 455 460
 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
 465 470 475 480
 Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
 485 490 495
 Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
 500 505 510

<210> 11
 <211> 1533
 <212> DNA
 <213> Glycine max

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 <211> 510
 <212> PRT
 <213> Glycine max

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 His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
 35 40 45

Val Asn Tyr Gln Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
 50 55 60
 Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
 65 70 75 80
 Val Ile Ala Asn Arg Glu Asp Ile Ser Trp Ala Thr Lys Asp Lys Ile
 85 90 95
 Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
 100 105 110
 Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
 115 120 125
 Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
 130 135 140
 Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
 145 150 155 160
 Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
 165 170 175
 Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
 180 185 190
 Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
 195 200 205
 Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
 210 215 220
 Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
 225 230 235 240
 Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
 245 250 255
 Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
 260 265 270
 Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
 275 280 285
 Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
 290 295 300
 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
 305 310 315 320
 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
 325 330 335
 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
 340 345 350
 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
 355 360 365
 Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
 370 375 380
 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
 385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
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Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

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<213> Glycine max

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<212> PRT
<213> Glycine max

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His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
 35 40 45
 Val Asn Tyr Gln Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
 50 55 60
 Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
 65 70 75 80
 Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
 85 90 95
 Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
 100 105 110
 Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
 115 120 125
 Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
 130 135 140
 Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
 145 150 155 160
 Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
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 Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
 180 185 190
 Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
 195 200 205
 Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
 210 215 220
 Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
 225 230 235 240
 Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
 245 250 255
 Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
 260 265 270
 Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
 275 280 285
 Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
 290 295 300
 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
 305 310 315 320
 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
 325 330 335
 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
 340 345 350
 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
 355 360 365
 Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
 370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
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Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
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Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
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<211> 1533
<212> DNA
<213> Glycine max

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cagtggattg tcaaacccaa atccgtcaac taccaattta aaaccaacac ccatgttcca 180
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<400> 16
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Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
 20 25 30
 His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
 35 40 45
 Val Asn Tyr Gln Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
 50 55 60
 Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
 65 70 75 80
 Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
 85 90 95
 Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
 100 105 110
 Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
 115 120 125
 Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
 130 135 140
 Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
 145 150 155 160
 Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
 165 170 175
 Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
 180 185 190
 Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
 195 200 205
 Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
 210 215 220
 Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
 225 230 235 240
 Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
 245 250 255
 Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
 260 265 270
 Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
 275 280 285
 Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
 290 295 300
 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
 305 310 315 320
 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
 325 330 335
 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
 340 345 350
 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
 355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510